

FIG. 1

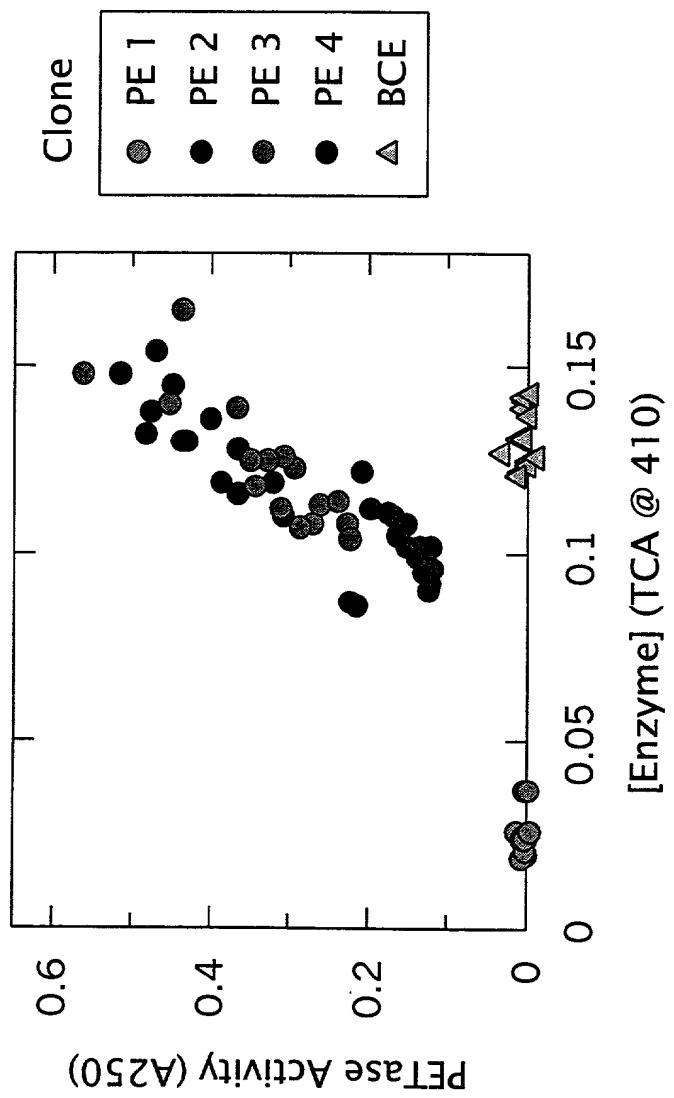


FIG. 2

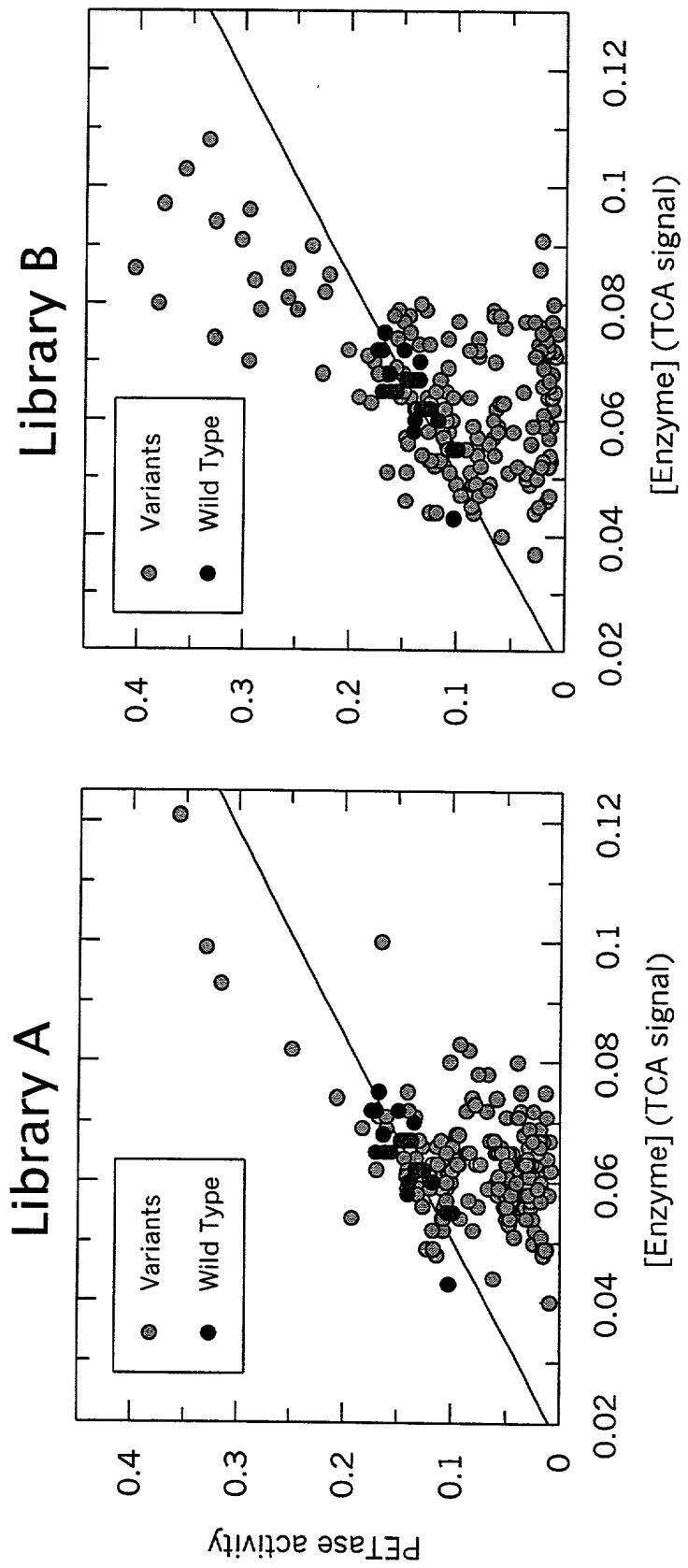


FIG. 3

1 FIG. 4

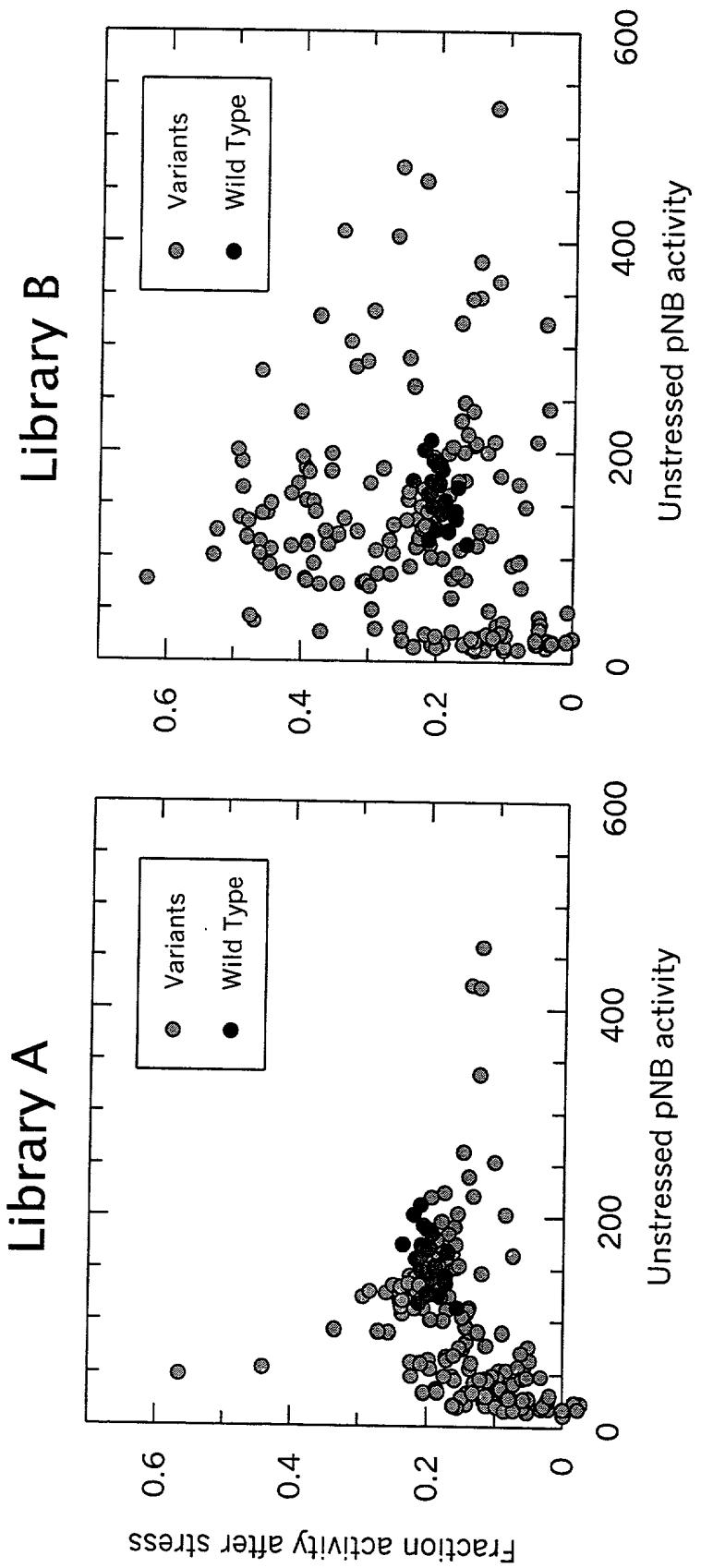


FIG. 5

FIG. 6

FIG. 8

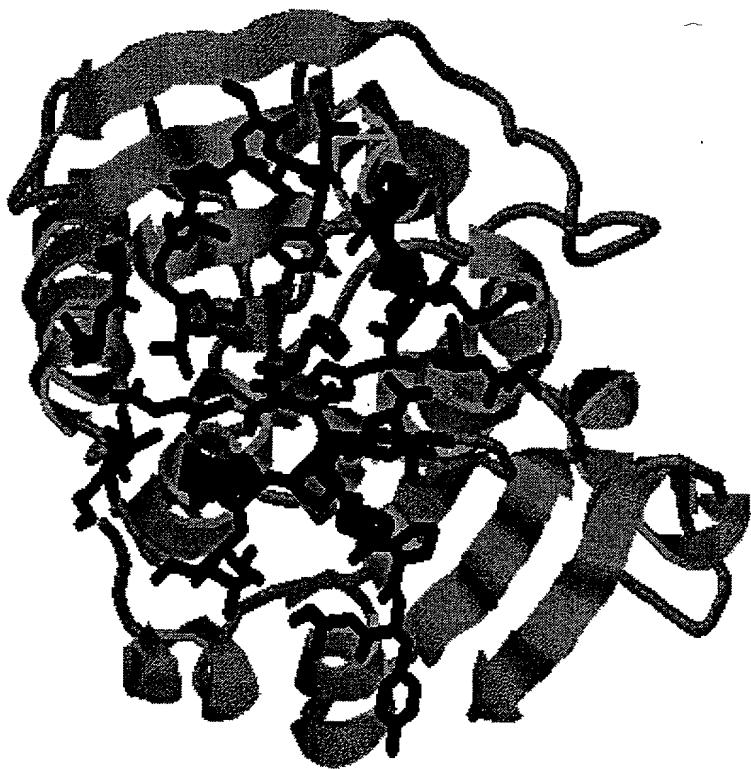
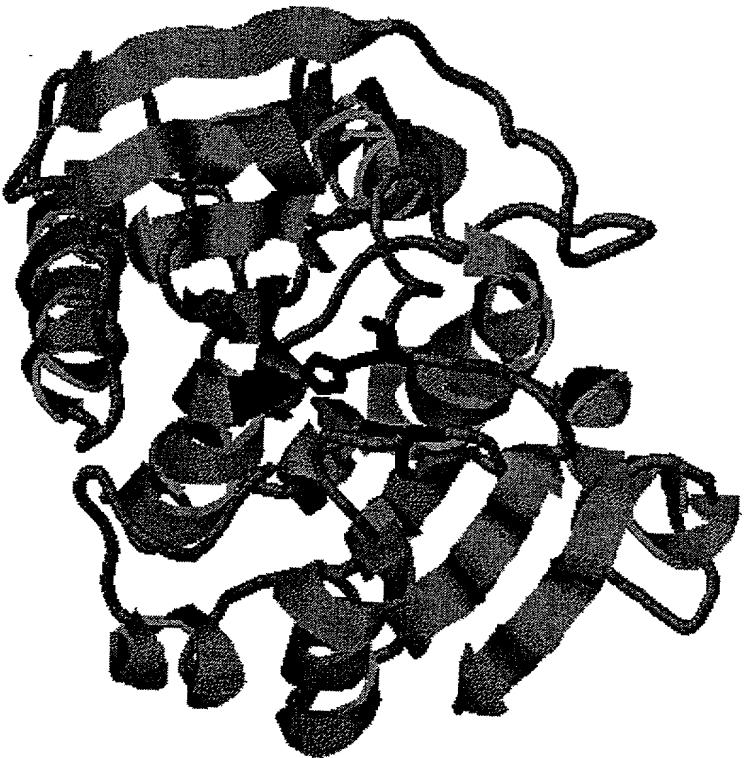
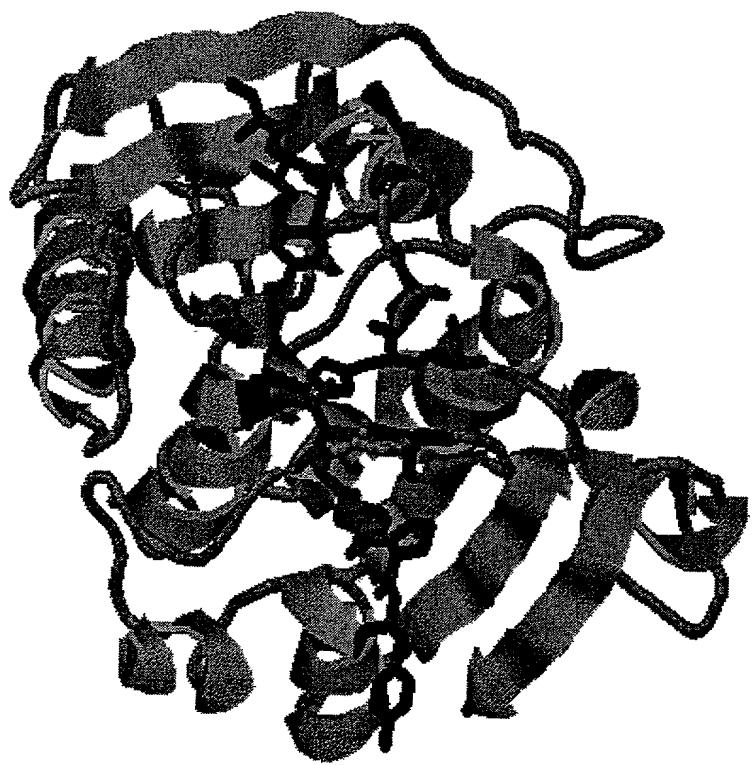


FIG. 7





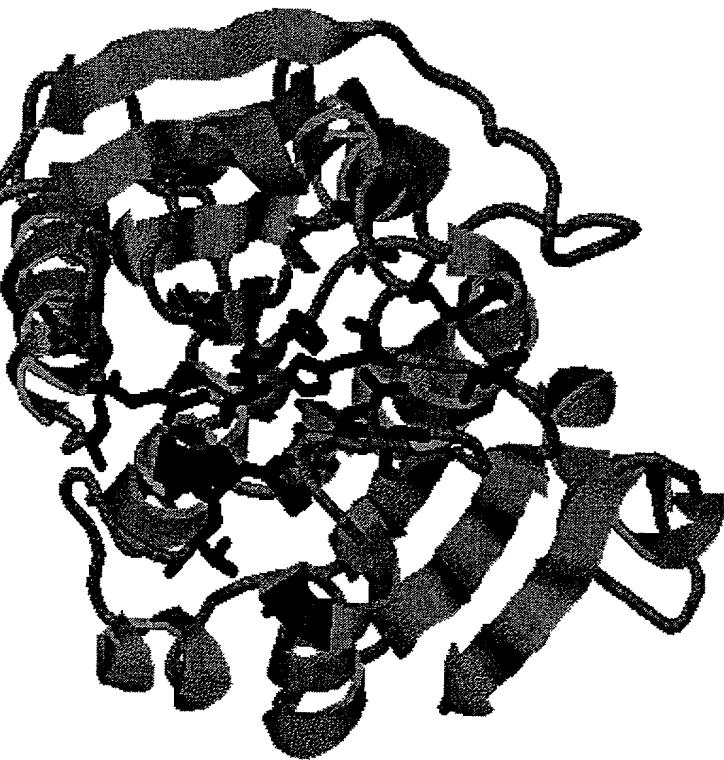


FIG. 11

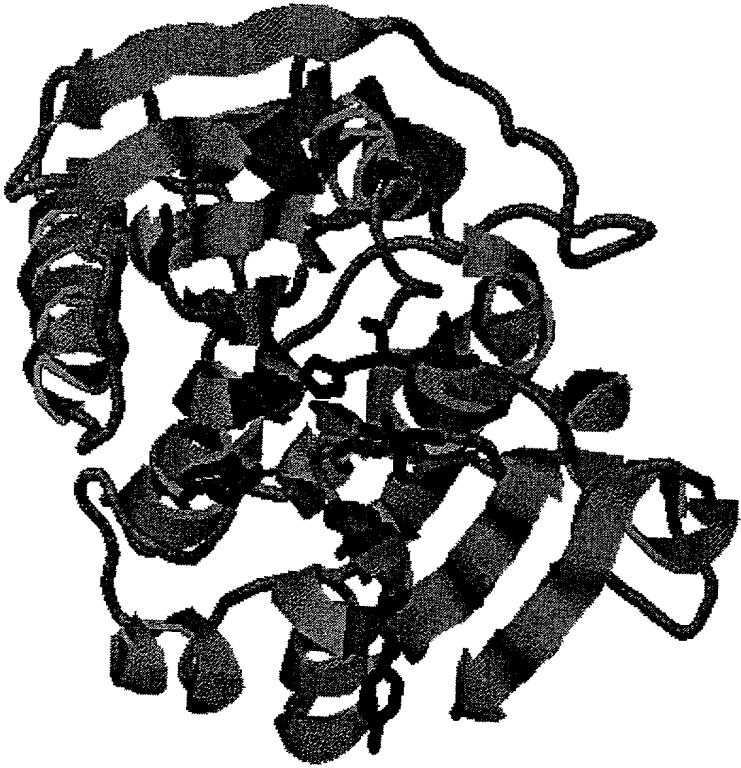


FIG. 12

FIG. 14

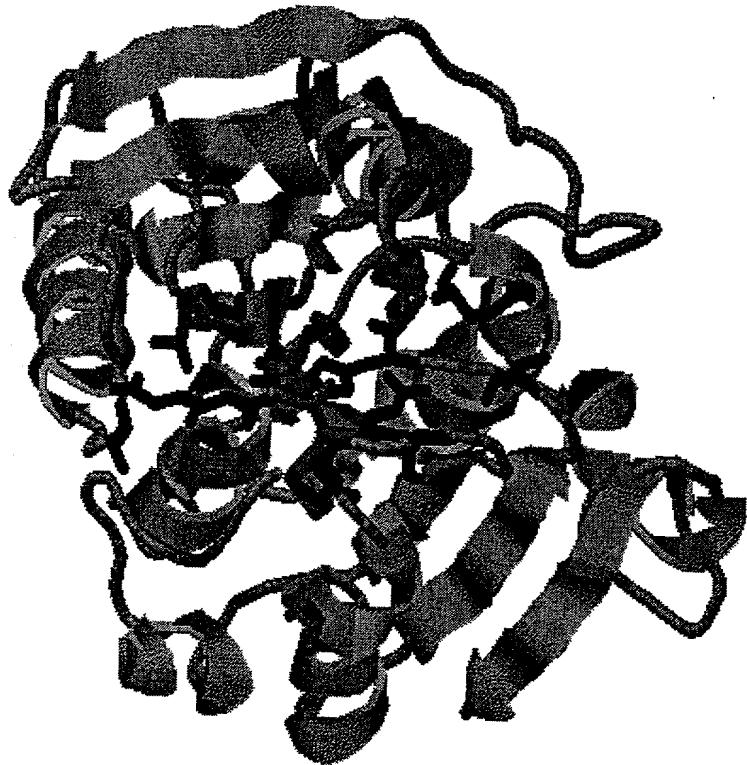
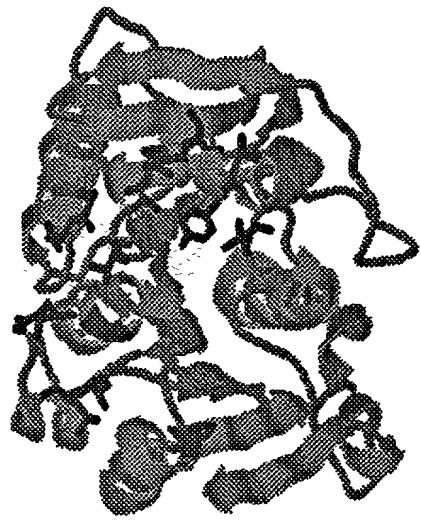


FIG. 13



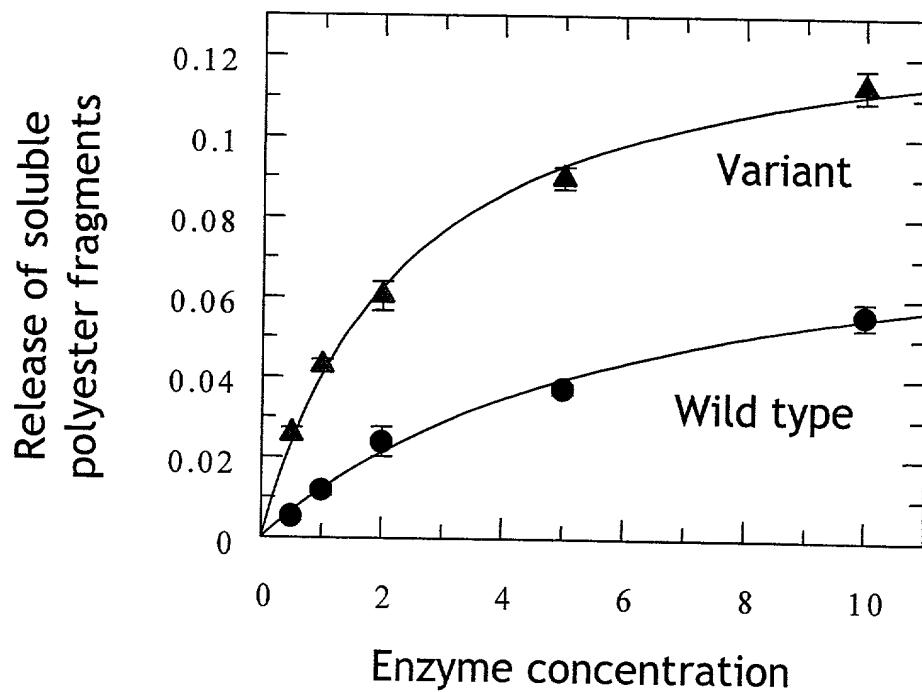


FIG. 15

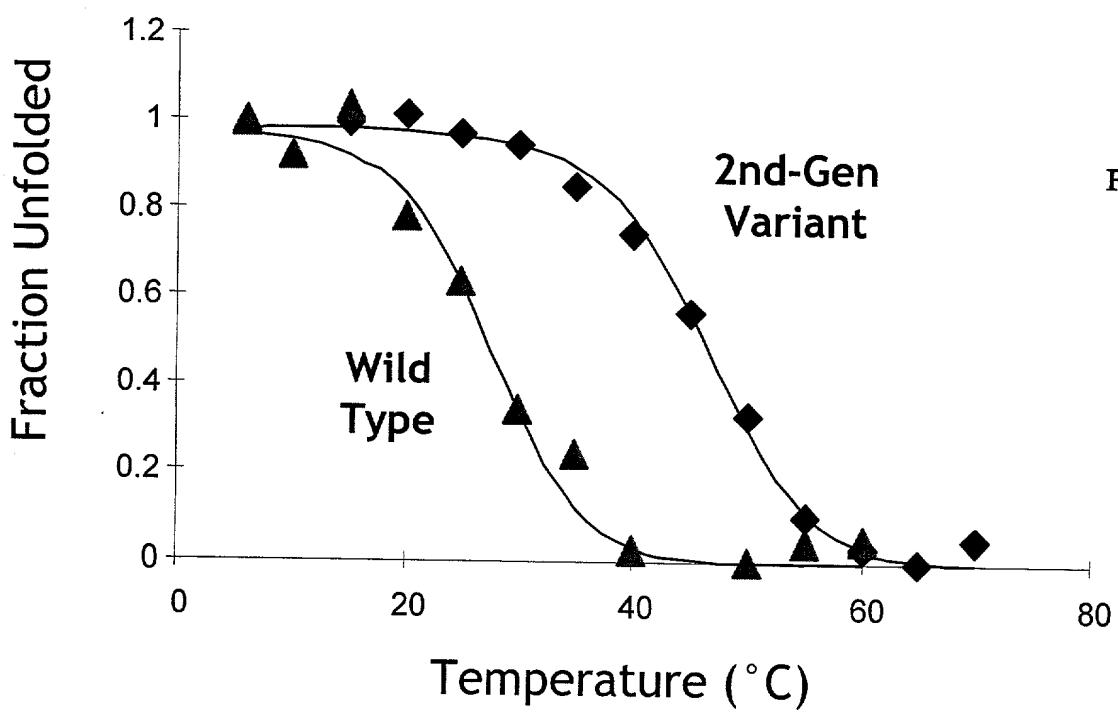


FIG. 16

Created: Tuesday, February 01, 2000 2:19 PM

10 20 30 40

TGGCGGCCTTGCCTGTCGTCTGTGCCACTGTCGGC 40
GGCTCCCTGCCGGATACACCGGGAGCGCCATTCCGGCT 80
GTCGCCAATTGACCGCAGTGGCCCTACACCAACAGCA 120
GCCAGAGCGAGGGGCCGAGCTGTCGATCTATCGGCCCCG 160
CGACCTGGGTAGGGGGCGTGCATCCGGTATTCTC 200

210 220 230 240

TGGGGCAATGGCACCGGTGCCGGCGTCCACCTATGCCG 240
GCTTGCTATCGCACTGGCAAGCCACGGTTCTGGTGGC 280
GCCGGCGGAAACCTCCAATGCCGGTACCGGGCGGGAAATG 320
CTGGCCTGCCCTGGACTATCTGGTACGTGAGAACGACACCC 360
CCTACGGCACCTATTCCGGCAAGCTCAATACCGGGCGAGT 400

410 420 430 440

CGGCACTTCTGGCATTCCCAGGGTGGTGGCGGCTCGATC 440
ATGGCCGGGCAGGATACGAGGGTGCCTACCGACGGCGCCGA 480
TCCAGCCCTACACCCCTGGCCTGGGCACGACAGCGCCTC 520
GAGCGGGCGGCAGCAGGGGCCGATGTTCTGATGTCCGGT 560
GGGGTGACACCATGCCCTTCCCTACCTCAACGCTCAGC 600

610 620 630 640

CGGTCTACCGGCGTCCAATGTGCCGGTGTCTGGGGCGA 640
ACGGCGTTACGTCAAGCCACTTCGAGCCGGTCGGTAGCGGT 680
GGGGCCTATCGCGGCCGAGCACGGCATGGTCCGCTTCC 720
AGCTGATGGATGACCAAGACGCCCCGCTACCTTCTACGG 760
CGCGCAGTGCAGTCTGTGCACCAAGCCTGCTGTGGTCGGTC 800

810 820 830 840

GAGCGCCGGCTTAA 818

Fig. 17

lipasewtgene Map.MPD (1 > 818) Site and Sequence

Enzymes : All 515 enzymes (No Filter)

Settings : Circular, Certain Sites Only, Standard Genetic Code

TGGCGGCCCTTGCGCTGCGTGTGCCACTGTCGCGCGGCTCCCTGCCGGATACACCGG 63
 Met Ala Ala Ser Cys Leu Ser Val Cys Ala Thr Val Ala Ala Ala Pro Leu Pro Asp Thr Pro

GAGCGCCATTCCGGCTGCGCAATTGACCGCAGTGGCCCTACACCACAGCAGCCAGA 126
 Gly Ala Pro Phe Pro Ala Val Ala Asn Phe Asp Arg Ser Gly Pro Tyr Thr Ser Ser Gln

GCGAGGGGCCGAGCTGTCGATCTATCGGCCCCGCGACCTGGGTCAAGGGGGCGTGCATC 189
 Ser Glu Gly Pro Ser Cys Arg Ile Tyr Arg Pro Arg Asp Leu Gly Gln Gly Val Arg His

CGGTGATTCTCTGGGGCAATGGCACCGGTGCCGGCCGTCCACCTATGCCGGCTTGCTATCGC 252
 Pro Val Ile Leu Trp Gly Asn Gly Thr Gly Ala Gly Pro Ser Thr Tyr Ala Gly Leu Leu Ser

ACTGGGCAAGCCACGGTTCTGGTGGCGGGCGGAAACCTCCAATGCCGGTACCGGGCGGG 315
 His Trp Ala Ser His Gly Phe Val Val Ala Ala Glu Thr Ser Asn Ala Gly Thr Gly Arg

AAATGCTCGCCTGCCTGGACTATCTGGTACGTGAGAACGACACCCCTACGGCACCTATTCCG 378
 Glu Met Leu Ala Cys Leu Asp Tyr Leu Val Arg Glu Asn Asp Thr Pro Tyr Gly Thr Tyr Ser

GCAAGCTCAATACCGGGCGAGTCGGCACTTCTGGCATTCCCAGGGTGGTGGCGGCTCGATCA 441
 Gly Lys Leu Asn Thr Gly Arg Val Gly Thr Ser Gly His Ser Gln Gly Gly Ser Ile

TGGCCGGGCAGGATACGAGGGTGCCTACCGCCGCGATCCAGCCCTACACCCCTGGCCTGG 504
 Met Ala Gly Gln Asp Thr Arg Val Arg Thr Thr Ala Pro Ile Gln Pro Tyr Thr Leu Gly Leu

GGCACGACAGCGCCTCGCAGCGCGGCAGCAGGGGCCATGTTCTGATGTCCGGTGGCGGTG 567
 Gly His Asp Ser Ala Ser Gln Arg Arg Gln Gln Gly Pro Met Phe Leu Met Ser Gly Gly Gly

ACACCATCGCCTTCCCTACCTCAACGCTCAGCCGGTCTACCGCGTGCCAATGTGCCGGTGT 630
 Asp Thr Ile Ala Phe Pro Tyr Leu Asn Ala Gln Pro Val Tyr Arg Arg Ala Asn Val Pro Val

TCTGGGGCGAACGGCGTTACGTCAAGCCACTTCGAGCCGGTGGTAGCGGTGGGCCTATCGCG 693
 Phe Trp Gly Glu Arg Arg Tyr Val Ser His Phe Glu Pro Val Gly Ser Gly Gly Ala Tyr Arg

GCCCCGAGCACGGCATGGTCCGCTTCCAGCTGATGGATGACCAAGACGCCCGCGCTACCTTCT 756
 Gly Pro Ser Thr Ala Trp Phe Arg Phe Gln Leu Met Asp Asp Gln Asp Ala Arg Ala Thr Phe

ACGGCGCGCAGTGCAGTCTGTGACCAAGCCTGCTGTGGTCGGTCAAGCGCCGCGGGCTTTAA 818
 Tyr Gly Ala Gln Cys Ser Leu Cys Thr Ser Leu Leu Trp Ser Val Glu Arg Arg Gly Leu •

Fig 18